Fig. 1A

```
  1 AGCATCCTGA GTAATGAGTG GCCTGGGCCG GAGCAGGCGA GGTGGCCGGA GCCGTGTGGA CCAGGAGGAG CGCTTTCCAC AGGGCCTGTG GACGGGGGTG
    TCGTAGGACT CATTACTCAC CGGACCCGGC CTCGTCCGCT CCACCGGCCT CGGCACACCT GGTCCTCCTC GCGAAAGGTG TCCCGGACAC CTGCCCCCAC
  1                M  S  G  L  G  R  S  R  R  G  G  R  S  R  V  D  Q  E  E  R  F  P  Q  G  L  W  T  G  V

101 GCTATGAGAT CCTGCCCCGA AGAGCAGTAC TGGGATCCTC TGCTGGGTAC CTGCATGTCC TGCAAAACCA TTTGCAACCA TCAGAGCCAG CGCACCTGTG
    CGATACTCTA GGACGGGGCT TCTCGTCATG ACCCTAGGAG ACGACCCATG GACGTACAGG ACGTTTTGGT AAACGTTGGT AGTCTCGGTC GCGTGGACAC
 30 A  M  R  S  C  P  E  E  Q  Y  W  D  P  L  L  G  T  C  M  S  C  K  T  I  C  N  H  Q  S  Q  R  T  C  A

201 CAGCCTTCTG CAGGTCACTC AGCTGCCGCA AGGAGCAAGG CAAGTTCTAT GACCATCTCC TGAGGGACTG CATCAGCTGT GCCTCCATCT GTGGACAGCA
    GTCGGAAGAC GTCCAGTGAG TCGACGGCGT TCCTCGTTCC GTTCAAGATA CTGGTAGAGG ACTCCCTGAC GTAGTCGACA CGGAGGTAGA CACCTGTCGT
 64  A  F  C  R  S  L  S  C  R  K  E  Q  G  K  F  Y  D  H  L  L  R  D  C  I  S  C  A  S  I  C  G  Q  H

301 CCCTAAGCAA TGTGCATACT TCTGTGAGAA CAAGCTCAGG AGCCCAGTGA ACCTTCCACC AGAGCTCAGG AGACAGCGGA GTGGAGAAGT TGAAAACAAT
    GGGATTCGTT ACACGTATGA AGACACTCTT GTTCGAGTCC TCGGGTCACT TGGAAGGTGG TCTCGAGTCC TCTGTCGCCT CACCTCTTCA ACTTTTGTTA
 97  P  K  Q  C  A  Y  F  C  E  N  K  L  R  S  P  V  N  L  P  P  E  L  R  R  Q  R  S  G  E  V  E  N  N

401 TCAGACAACT CGGGAAGGTA CCAAGGATTG GAGCACAGAG GCTCAGAAGC AAGTCCAGCT CTCCCGGGGC TGAAGCTGAG TGCAGATCAG GTGGCCCTGG
    AGTCTGTTGA GCCCTTCCAT GGTTCCTAAC CTCGTGTCTC CGAGTCTTCG TTCAGGTCGA GAGGGCCCCG ACTTCGACTC ACGTCTAGTC CACCGGGACC
130 S  D  N  S  G  R  Y  Q  G  L  E  H  R  G  S  E  A  S  P  A  L  P  G  L  K  L  S  A  D  Q  V  A  L  V

501 TCTACAGCAC GCTGGGGCTC TGCCTGTGTG CCGTCCTCTG CTGCTTCCTG GTGGCGGTGG CCTGCTTCCT CAAGAAGAGG GGGGATCCCT GCTCCTGCCA
    AGATGTCGTG CGACCCCGAG ACGGACACAC GGCAGGAGAC GACGAAGGAC CACCGCCACC GGACGAAGGA GTTCTTCTCC CCCCTAGGGA CGAGGACGGT
164  Y  S  T  L  G  L  C  L  C  A  V  L  C  C  F  L  V  A  V  A  C  F  L  K  K  R  G  D  P  C  S  C  Q

601 GCCCCGCTCA AGGCCCCGTC AAAGTCCGGC CAAGTCTTCC CAGGATCACG CGATGGAAGC CGGCAGCCCT GTGAGCACAT CCCCCGAGCC AGTGGAGACC
    CGGGGCGAGT TCCGGGGCAG TTTCAGGCCG GTTCAGAAGG GTCCTAGTGC GCTACCTTCG GCCGTCGGGA CACTCGTGTA GGGGGCTCGG TCACCTCTGG
197  P  R  S  R  P  R  Q  S  P  A  K  S  S  Q  D  H  A  M  E  A  G  S  P  V  S  T  S  P  E  P  V  E  T

701 TGCAGCTTCT GCTTCCCTGA GTGCAGGGCG CCCACGCAGG AGAGCGCAGT CACGCCTGGG ACCCCCGACC CCACTTGTGC TGGAAGGTGG GGGTGCCACA
    ACGTCGAAGA CGAAGGGACT CACGTCCCGC GGGTGCGTCC TCTCGCGTCA GTGCGGACCC TGGGGGCTGG GGTGAACACG ACCTTCCACC CCCACGGTGT
230 C  S  F  C  F  P  E  C  R  A  P  T  Q  E  S  A  V  T  P  G  T  P  D  P  T  C  A  G  R  W  G  C  H  T

801 CCAGGACCAC AGTCCTGCAG CCTTGCCCAC ACATCCCAGA CAGTGGCCTT GGCATTGTGT GTGTGCCTGC CCAGGAGGGG GGCCCAGGTG CATAAATGGG
    GGTCCTGGTG TCAGGACGTC GGAACGGGTG TGTAGGGTCT GTCACCGGAA CCGTAACACA CACACGGACG GGTCCTCCCC CCGGGTCCAC GTATTTACCC
264  R  T  T  V  L  Q  P  C  P  H  I  P  D  S  G  L  G  I  V  C  V  P  A  Q  E  G  G  P  G  A  O
```

```
901  GGTCAGGGAG GGAAAGGAGG AGGGAGAGAG ATGGAGAGGA GGGGAGAGAG AAAGAGAGGT GGGGAGAGGG GAGAGAGATA TGAGGAGAGA GAGACAGAGG
     CCAGTCCCTC CCTTTCCTCC TCCCTCTCTC TACCTCTCCT CCCCTCTCTC TTTCTCTCCA CCCCTCTCCC CTCTCTCTAT ACTCCTCTCT CTCTGTCTCC

1001 AGGCAGAAAG GGAGAGAAAC AGAGGAGACA GAGAGGGAGA GAGAGACAGA GGGAGAGAGA GACAGAGGGG AAGAGAGGCA GAGAGGGAAA GAGGCAGAGA
     TCCGTCTTTC CCTCTCTTTG TCTCCTCTGT CTCTCCCTCT CTCTCTGTCT CCCTCTCTCT CTGTCTCCCC TTCTCTCCGT CTCTCCCTTT CTCCGTCTCT

1101 AGGAAAGAGA CAGGCAGAGA AGGAGAGAGG CAGAGAGGGA GAGAGGCAGA GAGGGAGAGA GGCAGAGAGA CAGAGAGGGA GAGAGGGACA GAGAGAGATA
     TCCTTTCTCT GTCCGTCTCT TCCTCTCTCC GTCTCTCCCT CTCTCCGTCT CTCCCTCTCT CCGTCTCTCT GTCTCTCCCT CTCTCCCTGT CTCTCTCTAT

1201 GAGCAGGAGG TCGGGGCACT CTGAGTCCCA GTTCCCAGTG CAGCTGTAGG TCGTCATCAC CTAACCACAC GTGCAATAAA GTCCTCGTGC CTGCTGCTCA
     CTCGTCCTCC AGCCCCGTGA GACTCAGGGT CAAGGGTCAC GTCGACATCC AGCAGTAGTG GATTGGTGTG CACGTTATTT CAGGAGCACG GACGACGAGT

1301 CAGCCCCCGA GAGCCCCTCC TCCTGGAGAA TAAAACCTTT GGCAGCTGCC CTTCCTCAAA AAAAAAAAAA AAAAAAA
     GTCGGGGGCT CTCGGGGAGG AGGACCTCTT ATTTTGGAAA CCGTCGACGG GAAGGAGTTT TTTTTTTTTT TTTTTTT
```

Fig. 1B

Fig. 2

```
  1 AAGACTCAAA CTTAGAAACT TGAATTAGAT GTGGTATTCA AATCCTTACG TGCCGCGAAG ACACAGACAG CCCCCGTAAG AACCCACGAA GCAGGCGAAG
    TTCTGAGTTT GAATCTTTGA ACTTAATCTA CACCATAAGT TTAGGAATGC ACGGCGCTTC TGTGTCTGTC GGGGGCATTC TTGGGTGCTT CGTCCGCTTC

101 TTCATTGTTC TCAACATTCT AGCTGCTCTT GCTGCATTTG CTCTGGAATT CTTGTAGAGA TATTACTTGT CCTTCCAGGC TGTTCTTTCT GTAGCTCCCT
    AAGTAACAAG AGTTGTAAGA TCGACGAGAA CGACGTAAAC GAGACCTTAA GAACATCTCT ATAATGAACA GGAAGGTCCG ACAAGAAAGA CATCGAGGGA

201 TGTTTTCTTT TTGTGATCAT GTTGCAGATG GCTGGGCAGT GCTCCCAAAA TGAATATTTT GACAGTTTGT TGCATGCTTG CATACCTTGT CAACTTCGAT
    ACAAAAGAAA AACACTAGTA CAACGTCTAC CGACCCGTCA CGAGGGTTTT ACTTATAAAA CTGTCAAACA ACGTACGAAC GTATGGAACA GTTGAAGCTA
  1                    Me tLeuGlnMet AlaGlyGlnC ysSerGlnAs nGluTyrPhe AspSerLeuL euHisAlaCy sIleProCys GlnLeuArgC

301 GTTCTTCTAA TACTCCTCCT CTAACATGTC AGCGTTATTG TAATGCAAGT GTGACCAATT CAGTGAAAGG AACGAATGCG ATTCTCTGGA CCTGTTTGGG
    CAAGAAGATT ATGAGGAGGA GATTGTACAG TCGCAATAAC ATTACGTTCA CACTGGTTAA GTCACTTTCC TTGCTTACGC TAAGAGACCT GGACAAACCC
 29 ysSerSerAs nThrProPro LeuThrCysG lnArgTyrCy sAsnAlaSer ValThrAsnS erValLysGl yThrAsnAla IleLeuTrpT hrCysLeuGl

401 ACTGAGCTTA ATAATTTCTT TGGCAGTTTT CGTGCTAATG TTTTTGCTAA GGAAGATAAG CTCTGAACCA TTAAAGGACG AGTTTAAAAA CACAGGATCA
    TGACTCGAAT TATTAAAGAA ACCGTCAAAA GCACGATTAC AAAAACGATT CCTTCTATTC GAGACTTGGT AATTTCCTGC TCAAATTTTT GTGTCCTAGT
 62 yLeuSerLeu IleIleSerL euAlaValPh eValLeuMet PheLeuLeuA rgLysIleSe rSerGluPro LeuLysAspG luPheLysAs nThrGlySer

501 GGTCTCCTGG GCATGGCTAA CATTGACCTG GAAAAGAGCA GGACTGGTGA TGAAATTATT CTTCCGAGAG GCCTCGAGTA CACGGTGGAA GAATGCACCT
    CCAGAGGACC CGTACCGATT GTAACTGGAC CTTTTCTCGT CCTGACCACT ACTTTAATAA GAAGGCTCTC CGGAGCTCAT GTGCCACCTT CTTACGTGGA
 95 GlyLeuLeuG lyMetAlaAs nIleAspLeu GluLysSerA rgThrGlyAs pGluIleIle LeuProArgG lyLeuGluTy rThrValGlu GluCysThrC

601 GTGAAGACTG CATCAAGAGC AAACCGAAGG TCGACTCTGA CCATTGCTTT CCACTCCCAG CTATGGAGGA AGGCGCAACC ATTCTTGTCA CCACGAAAAC
    CACTTCTGAC GTAGTTCTCG TTTGGCTTCC AGCTGAGACT GGTAACGAAA GGTGAGGGTC GATACCTCCT TCCGCGTTGG TAAGAACAGT GGTGCTTTTG
129 ysGluAspCy sIleLysSer LysProLysV alAspSerAs pHisCysPhe ProLeuProA laMetGluGl uGlyAlaThr IleLeuValT hrThrLysTh

701 GAATGACTAT TGCAAGAGCC TGCCAGCTGC TTTGAGTGCT ACGGAGATAG AGAAATCAAT TTCTGCTAGG TAATTAACCA TTTCGACTCG AGCAGTGCCA
    CTTACTGATA ACGTTCTCGG ACGGTCGACG AAACTCACGA TGCCTCTATC TCTTTAGTTA AAGACGATCC ATTAATTGGT AAAGCTGAGC TCGTCACGGT
162 rAsnAspTyr CysLysSerL euProAlaAl aLeuSerAla ThrGluIleG luLysSerIl eSerAlaArg OC*

801 CTTTAAAAAT CTTTTGTCAG AATAGATGAT GTGTCAGATC TCTTTAGGAT GACTGTATTT TTCAGTTGCC GATACAGCTT TTTGTCCTCT AACTGTGGAA
    GAAATTTTTA GAAAACAGTC TTATCTACTA CACAGTCTAG AGAAATCCTA CTGACATAAA AAGTCAACGG CTATGTCGAA AAACAGGAGA TTGACACCTT

901 ACTCTTTATG TTAGATATAT TTCTCTAGGT TACTGTTGGG AGCTTAATGG TAGAAACTTC CTTGGTTTCA TGATTAAAGT CTTTTTTTTT CCTGA
    TGAGAAATAC AATCTATATA AAGAGATCCA ATGACAACCC TCGAATTACC ATCTTTGAAG GAACCAAAGT ACTAATTTCA GAAAAAAAAA GGACT
```

Fig. 3

```
  1 ATGGATGACT CCACAGAAAG GGAGCAGTCA CGCCTTACTT CTTGCCTTAA GAAAAGAGAA GAAATGAAAC TGAAGGAGTG TGTTTCCATC CTCCCACGGA
    TACCTACTGA GGTGTCTTTC CCTCGTCAGT GCGGAATGAA GAACGGAATT CTTTTCTCTT CTTTACTTTG ACTTCCTCAC ACAAAGGTAG GAGGGTGCCT
  1 M  D  D  S   T  E  R   E  Q  S   R  L  T  S   C  L  K   K  R  E   E  M  K  L   K  E  C   V  S  I   L  P  R  K

101 AGGAAAGCCC CTCTGTCCGA TCCTCCAAAG ACGGAAAGCT GCTGGCTGCA ACCTTGCTGC TGGCACTGCT GTCTTGCTGC CTCACGGTGG TGTCTTTCTA
    TCCTTTCGGG GAGACAGGCT AGGAGGTTTC TGCCTTTCGA CGACCGACGT TGGAACGACG ACCGTGACGA CAGAACGACG GAGTGCCACC ACAGAAAGAT
 35  E  S  P   S  V  R   S  S  K  D   G  K  L   L  A  A   T  L  L  L   A  L  L   S  C  C   L  T  V  V   S  F  Y

201 CCAGGTGGCC GCCCTGCAAG GGGACCTGGC CAGCCTCCGG GCAGAGCTGC AGGGCCACCA CGCGGAGAAG CTGCCAGCAG GAGCAGGAGC CCCCAAGGCC
    GGTCCACCGG CGGGACGTTC CCCTGGACCG GTCGGAGGCC CGTCTCGACG TCCCGGTGGT GCGCCTCTTC GACGGTCGTC CTCGTCCTCG GGGGTTCCGG
 68 Q  V  A   A  L  Q  G   D  L  A   S  L  R   A  E  L  Q   G  H  H   A  E  K   L  P  A  G   A  G  A   P  K  A

301 GGCTTGGAGG AAGCTCCAGC TGTCACCGCG GGACTGAAAA TCTTTGAACC ACCAGCTCCA GGAGAAGGCA ACTCCAGTCA GAACAGCAGA AATAAGCGTG
    CCGAACCTCC TTCGAGGTCG ACAGTGGCGC CCTGACTTTT AGAAACTTGG TGGTCGAGGT CCTCTTCCGT TGAGGTCAGT CTTGTCGTCT TTATTCGCAC
101 G  L  E  E   A  P  A   V  T  A   G  L  K  I   F  E  P   P  A  P   G  E  G  N   S  S  Q   N  S  R   N  K  R  A

401 CCGTTCAGGG TCCAGAAGAA ACAGTCACTC AAGACTGCTT GCAACTGATT GCAGACAGTG AAACACCAAC TATACAAAAA GGATCTTACA CATTTGTTCC
    GGCAAGTCCC AGGTCTTCTT TGTCAGTGAG TTCTGACGAA CGTTGACTAA CGTCTGTCAC TTTGTGGTTG ATATGTTTTT CCTAGAATGT GTAAACAAGG
135  V  Q  G   P  E  E   T  V  T  Q   D  C  L   Q  L  I   A  D  S  E   T  P  T   I  Q  K   G  S  Y  T   F  V  P

501 ATGGCTTCTC AGCTTTAAAA GGGGAAGTGC CCTAGAAGAA AAAGAGAATA AAATATTGGT CAAAGAAACT GGTTACTTTT TTATATATGG TCAGGTTTTA
    TACCGAAGAG TCGAAATTTT CCCCTTCACG GGATCTTCTT TTTCTCTTAT TTTATAACCA GTTTCTTTGA CCAATGAAAA AATATATACC AGTCCAAAAT
168 W  L  L   S  F  K  R   G  S  A   L  E  E   K  E  N  K   I  L  V   K  E  T   G  Y  F  F   I  Y  G   Q  V  L

601 TATACTGATA AGACCTACGC CATGGGACAT CTAATTCAGA GGAAGAAGGT CCATGTCTTT GGGGATGAAT TGAGTCTGGT GACTTTGTTT CGATGTATTC
    ATATGACTAT TCTGGATGCG GTACCCTGTA GATTAAGTCT CCTTCTTCCA GGTACAGAAA CCCCTACTTA ACTCAGACCA CTGAAACAAA GCTACATAAG
201 Y  T  D  K   T  Y  A   M  G  H   L  I  Q  R   K  K  V   H  V  F   G  D  E  L   S  L  V   T  L  F   R  C  I  Q

701 AAAATATGCC TGAAACACTA CCCAATAATT CCTGCTATTC AGCTGGCATT GCAAAACTGG AAGAAGGAGA TGAACTCCAA CTTGCAATAC CAAGAGAAAA
    TTTTATACGG ACTTTGTGAT GGGTTATTAA GGACGATAAG TCGACCGTAA CGTTTTGACC TTCTTCCTCT ACTTGAGGTT GAACGTTATG GTTCTCTTTT
235  N  M  P   E  T  L   P  N  N  S   C  Y  S   A  G  I   A  K  L  E   E  G  D   E  L  Q   L  A  I  P   R  E  N

801 TGCACAAATA TCACTGGATG GAGATGTCAC ATTTTTTGGT GCATTGAAAC TGCTGTGA
    ACGTGTTTAT AGTGACCTAC CTCTACAGTG TAAAAAACCA CGTAACTTTG ACGACACT
268 A  Q  I   S  L  D  G   D  V  T   F  F  G   A  L  K  L   L  O
```

00822TT"T4E42460

Fig. 4A

```
  1 GGTACGAGGC TTCCTAGAGG GACTGGAACC TAATTCTCCT GAGGCTGAGG GAGGGTGGAG GGTCTCAAGG CAACGCTGGC CCCACGACGG AGTGCCAGGA
    CCATGCTCCG AAGGATCTCC CTGACCTTGG ATTAAGAGGA CTCCGACTCC CTCCCACCTC CCAGAGTTCC GTTGCGACCG GGGTGCTGCC TCACGGTCCT

101 GCACTAACAG TACCCTTAGC TTGCTTTCCT CCTCCCTCCT TTTTATTTTC AAGTTCCTTT TTATTTCTCC TTGCGTAACA ACCTTCTTCC CTTCTGCACC
    CGTGATTGTC ATGGGAATCG AACGAAAGGA GGAGGGAGGA AAAATAAAAG TTCAAGGAAA AATAAAGAGG AACGCATTGT TGGAAGAAGG GAAGACGTGG

201 ACTGCCCGTA CCCTTACCCG CCCCGCCACC TCCTTGCTAC CCCACTCTTG AAACCACAGC TGTTGGCAGG GTCCCCAGCT CATGCCAGCC TCATCTCCTT
    TGACGGGCAT GGGAATGGGC GGGGCGGTGG AGGAACGATG GGGTGAGAAC TTTGGTGTCG ACAACCGTCC CAGGGGTCGA GTACGGTCGG AGTAGAGGAA
  1                                                                                        M  P  A   S  S  P  F

301 TCTTGCTAGC CCCCAAAGGG CCTCCAGGCA ACATGGGGGG CCCAGTCAGA GAGCCGGCAC TCTCAGTTGC CCTCTGGTTG AGTTGGGGGG CAGCTCTGGG
    AGAACGATCG GGGGTTTCCC GGAGGTCCGT TGTACCCCCC GGGTCAGTCT CTCGGCCGTG AGAGTCAACG GGAGACCAAC TCAACCCCCC GTCGAGACCC
  8  L  L  A   P  K  G   P  P  G  N   M  G  G   P  V  R   E  P  A  L   S  V  A   L  W  L   S  W  G  A   A  L  G

401 GGCCGTGGCT TGTGCCATGG CTCTGCTGAC CCAACAAACA GAGCTGCAGA GCCTCAGGAG AGAGGTGAGC CGGCTGCAGG GGACAGGAGG CCCCTCCCAG
    CCGGCACCGA ACACGGTACC GAGACGACTG GGTTGTTTGT CTCGACGTCT CGGAGTCCTC TCTCCACTCG GCCGACGTCC CCTGTCCTCC GGGGAGGGTC
 41  A  V  A   C  A  M  A   L  L  T   Q  Q  T   E  L  Q  S   L  R  R   E  V  S   R  L  Q  G   T  G  G   P  S  Q

501 AATGGGGAAG GGTATCCCTG GCAGAGTCTC CCGGAGCAGA GTTCCGATGC CCTGGAAGCC TGGGAGAATG GGGAGAGATC CCGGAAAAGG AGAGCAGTGC
    TTACCCCTTC CCATAGGGAC CGTCTCAGAG GGCCTCGTCT CAAGGCTACG GGACCTTCGG ACCCTCTTAC CCCTCTCTAG GGCCTTTTCC TCTCGTCACG
 74 N  G  E  G   Y  P  W   Q  S  L   P  E  Q  S   S  D  A   L  E  A   W  E  N  G   E  R  S   R  K  R   R  A  V  L

601 TCACCCAAAA ACAGAAGAAG CAGCACTCTG TCCTGCACCT GGTTCCCATT AACGCCACCT CCAAGGATGA CTCCGATGTG ACAGAGGTGA TGTGGCAACC
    AGTGGGTTTT TGTCTTCTTC GTCGTGAGAC AGGACGTGGA CCAAGGGTAA TTGCGGTGGA GGTTCCTACT GAGGCTACAC TGTCTCCACT ACACCGTTGG
108  T  Q  K   Q  K  K   Q  H  S  V   L  H  L   V  P  I   N  A  T  S   K  D  D   S  D  V   T  E  V  M   W  Q  P

701 AGCTCTTAGG CGTGGGAGAG GCCTACAGGC CCAAGGATAT GGTGTCCGAA TCCAGGATGC TGGAGTTTAT CTGCTGTATA GCCAGGTCCT GTTTCAAGAC
    TCGAGAATCC GCACCCTCTC CGGATGTCCG GGTTCCTATA CCACAGGCTT AGGTCCTACG ACCTCAAATA GACGACATAT CGGTCCAGGA CAAAGTTCTG
141  A  L  R   R  G  R  G   L  Q  A   Q  G  Y   G  V  R  I   Q  D  A   G  V  Y   L  L  Y  S   Q  V  L   F  Q  D

801 GTGACTTTCA CCATGGGTCA GGTGGTGTCT CGAGAAGGCC AAGGAAGGCA GGAGACTCTA TTCCGATGTA TAAGAAGTAT GCCCTCCCAC CCGGACCGGG
    CACTGAAAGT GGTACCCAGT CCACCACAGA GCTCTTCCGG TTCCTTCCGT CCTCTGAGAT AAGGCTACAT ATTCTTCATA CGGGAGGGTG GGCCTGGCCC
174 V  T  F  T   M  G  Q   V  V  S   R  E  G  Q   G  R  Q   E  T  L   F  R  C  I   R  S  M   P  S  H   P  D  R  A

901 CCTACAACAG CTGCTATAGC GCAGGTGTCT TCCATTTACA CCAAGGGGAT ATTCTGAGTG TCATAATTCC CCGGGCAAGG GCGAAACTTA ACCTCTCTCC
    GGATGTTGTC GACGATATCG CGTCCACAGA AGGTAAATGT GGTTCCCCTA TAAGACTCAC AGTATTAAGG GGCCCGTTCC CGCTTTGAAT TGGAGAGAGG
208  Y  N  S   C  Y  S   A  G  V  F   H  L  H   Q  G  D   I  L  S  V   I  I  P   R  A  R   A  K  L  N   L  S  P
```

```
1001 ACATGGAACC TTCCTGGGGT TTGTGAAACT GTGATTGTGT TATAAAAAGT GGCTCCCAGC TTGGAAGACC AGGGTGGGTA CATACTGGAG ACAGCCAAGA
     TGTACCTTGG AAGGACCCCA AACACTTTGA CACTAACACA ATATTTTTCA CCGAGGGTCG AACCTTCTGG TCCCACCCAT GTATGACCTC TGTCGGTTCT
 241  H  G  T   F  L  G  F   V  K  L   O

1101 GCTGAGTATA TAAAGGAGAG GGAATGTGCA GGAACAGAGG CATCTTCCTG GGTTTGGCTC CCCGTTCCTC ACTTTTCCCT TTTCATTCCC ACCCCCTAGA
     CGACTCATAT ATTTCCTCTC CCTTACACGT CCTTGTCTCC GTAGAAGGAC CCAAACCGAG GGGCAAGGAG TGAAAAGGGA AAAGTAAGGG TGGGGGATCT

1201 CTTTGATTTT ACGGATATCT TGCTTCTGTT CCCCATGGAG CTCCGAATTC TTGCGTGTGT GTAGATGAGG GGCGGGGGAC GGGCGCCAGG CATTGTTCAG
     GAAACTAAAA TGCCTATAGA ACGAAGACAA GGGGTACCTC GAGGCTTAAG AACGCACACA CATCTACTCC CCGCCCCCTG CCCGCGGTCC GTAACAAGTC

1301 ACCTGGTCGG GGCCCACTGG AAGCATCCAG AACAGCACCA CCATCTTA
     TGGACCAGCC CCGGGTGACC TTCGTAGGTC TTGTCGTGGT GGTAGAAT
```

Fig. 4B

FIGURE 5A

PRO	XXXXXXXXXXXXXXX	(Length = 15 amino acids)
Comparison Protein	XXXXXYYYYYYY	(Length = 12 amino acids)

% amino acid sequence identity =

(the number of identically matching amino acid residues between the two polypeptide sequences as determined by ALIGN-2) divided by (the total number of amino acid residues of the PRO polypeptide) =

5 divided by 15 = 33.3%

FIGURE 5B

PRO	XXXXXXXXXX	(Length = 10 amino acids)
Comparison Protein	XXXXXYYYYYYZZYZ	(Length = 15 amino acids)

% amino acid sequence identity =

(the number of identically matching amino acid residues between the two polypeptide sequences as determined by ALIGN-2) divided by (the total number of amino acid residues of the PRO polypeptide) =

5 divided by 10 = 50%

Fig. 6

```
                    10        20        30        40        50
hTACI (265)  MSGLGRSRRGGRSRVDQEERFPQGLWTGVAMRSCPEEQYWDPLLGTCMSC
hTACI.       MSGLGRSRRGGRSRVDQEERFPQGLWTGVAMRSCPEEQYWDPLLGTCMSC

                    60        70        80        90       100
hTACI (265)  KTICNHQSQRTCAAFCRSLSCRKEQGKFYDHLLRDCISCASICGQHPKQC
hTACI.       KTICNHQSQRTCAAFCRSLSCRKEQGKFYDHLLRDCISCASICGQHPKQC

                   110       120       130       140       150
hTACI (265)  AYFCENKLRSPVNLPPELRRQRSGEVENNSDNSGRYQGLEHRGSEASPAL
hTACI.       AYFCENKLRSPVNLPPELRRQRSGEVENNSDNSGRYQGLEHRGSEASPAL

                   160       170       180       190       200
hTACI (265)  PGLKLSADQVALVYSTLGLCLCAVLCCFLVAVACFLKKRGDPCSCQPRSR
hTACI.       PGLKLSADQVALVYSTLGLCLCAVLCCFLVAVACFLKKRGDPCSCQPRSR

                   210       220       230       240       250
hTACI (265)  PRQSPAKSSQDHAMEAGSPVSTSPEPVETCSFCFPECRAPTQESAVTPGT
hTACI.       PRQSPAKSSQDHAMEAGSPVSTSPEPVETCSFCFPECRAPTQESAVTPGT

                   260       270       280       290       300
hTACI (265)  PDPTCAGRT------------------------APPREG----Z
hTACI.       PDPTCAGRWGCHTRTTVLQPCPHIPDSGLGIVCVPAQEGGPGAZ
```

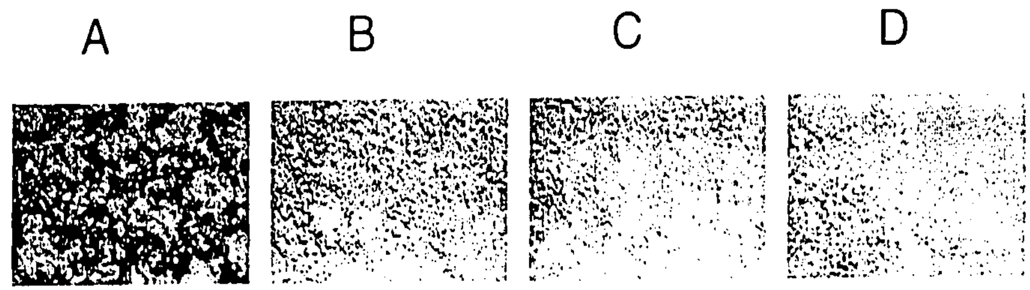


Fig. 7

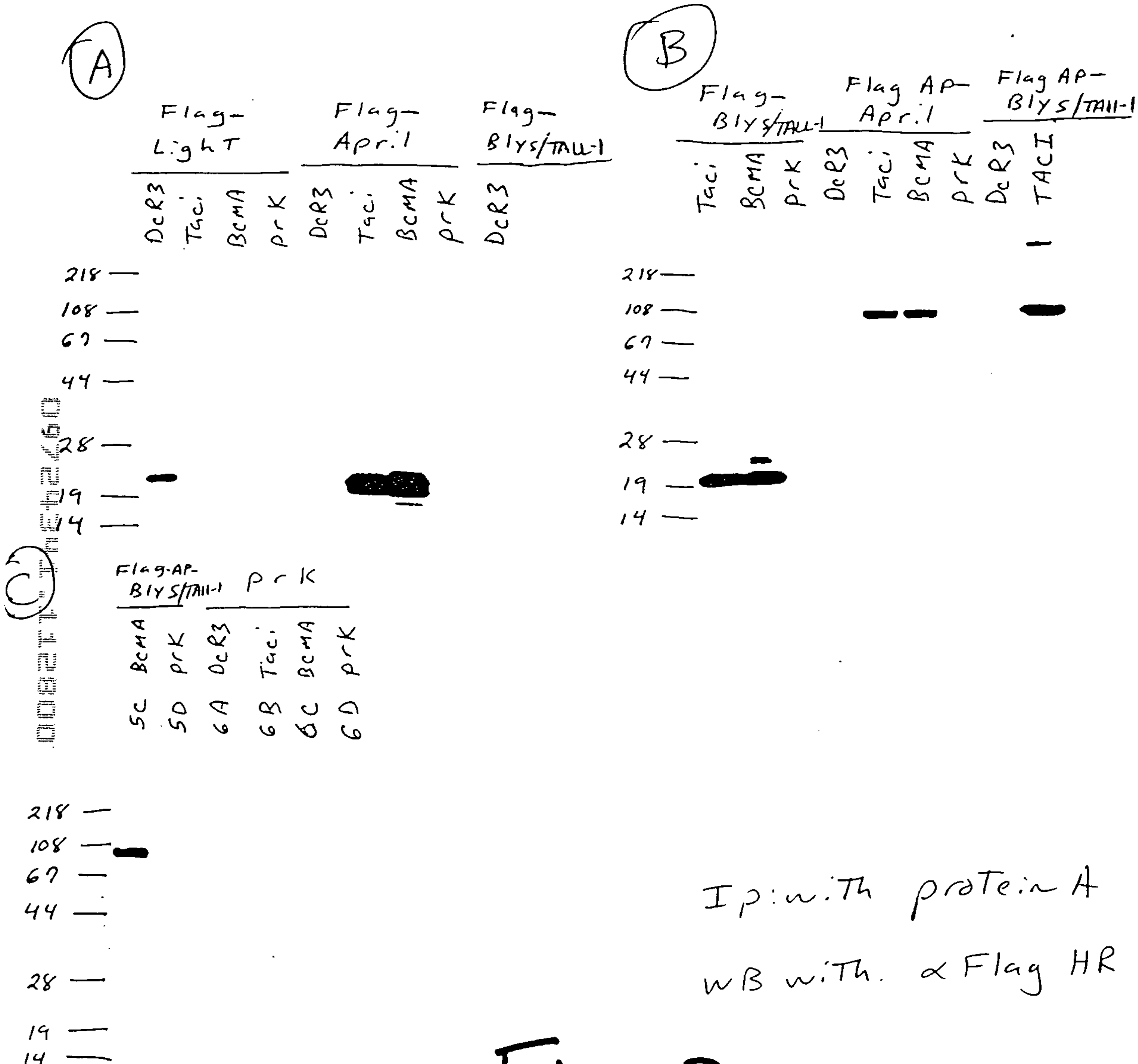

A
Flag-LighT
DcR3
Taci
BcMA
prK
Flag-April
DcR3
Taci
BCMA
prK
Flag-Blys/TALL-1
DcR3
218
108
67
44
28
19
14
B
Flag-Blys/TALL-1
Taci
BCMA
prK
DcR3
Flag AP-April
Taci
BCMA
prK
DcR3
Flag AP-Blys/TALL-1
TACI
C
Flag-AP-Blys/TALL-1
BcMA
prK
prK
DcR3
Taci
BCMA
prK
5C
5D
6A
6B
6C
6D
Ip: with protein A
WB with αFlag HR

Fig. 8

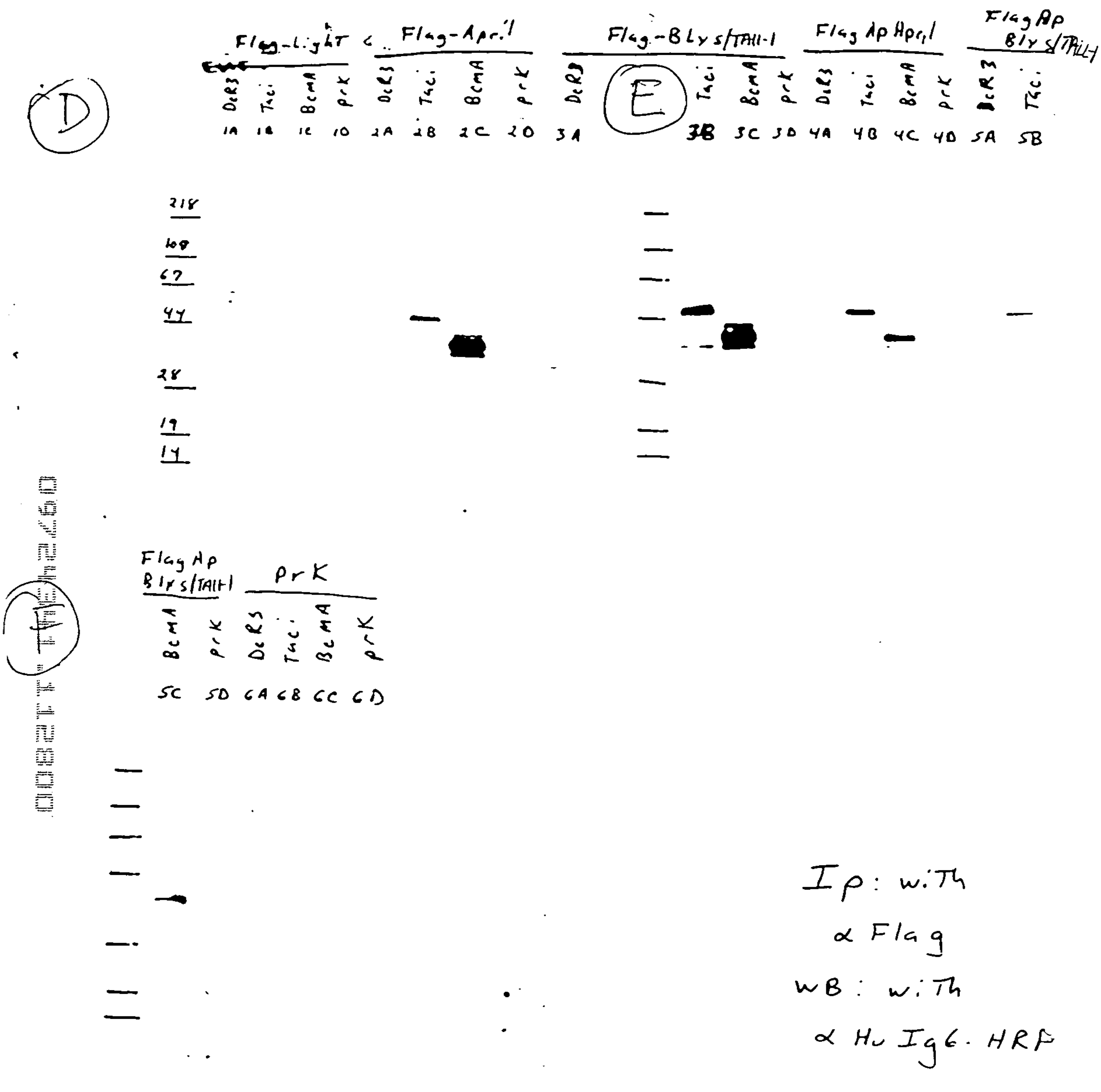

D
Flag-Light
Flag-April
DcR3 Taci BcmA prk DcR3 Taci BcmA prk
1A 1B 1C 1D 2A 2B 2C 2D
Flag-Blys/TALL-1
E
DcR3 Taci BcmA prk
3A 3B 3C 3D
Flag Ap April
DcR3 Taci BcmA prk
4A 4B 4C 4D
Flag Ap Blys/TALL-1
DcR3 Taci
5A 5B
218
108
67
44
28
19
14
F
Flag Ap Blys/TALL-1
prK
BcmA prk DcRs Taci BcmA prK
5C 5D 6A 6B 6C 6D
Ip: with
α Flag
WB: with
α Hu IgG-HRP

Fig. 8

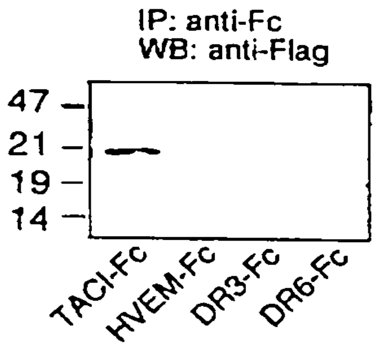

IP: anti-Fc
WB: anti-Flag
47
21
19
14
TACI-Fc
HVEM-Fc
DR3-Fc
DR6-Fc

Fig. 8G

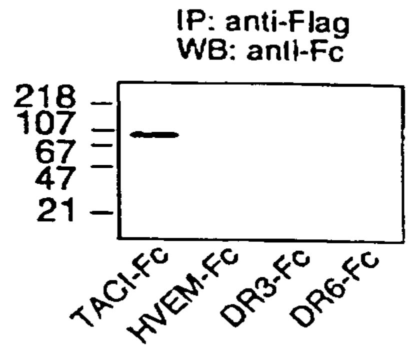

IP: anti-Flag
WB: anti-Fc
218
107
67
47
21
TACI-Fc
HVEM-Fc
DR3-Fc
DR6-Fc

Fig. 8H

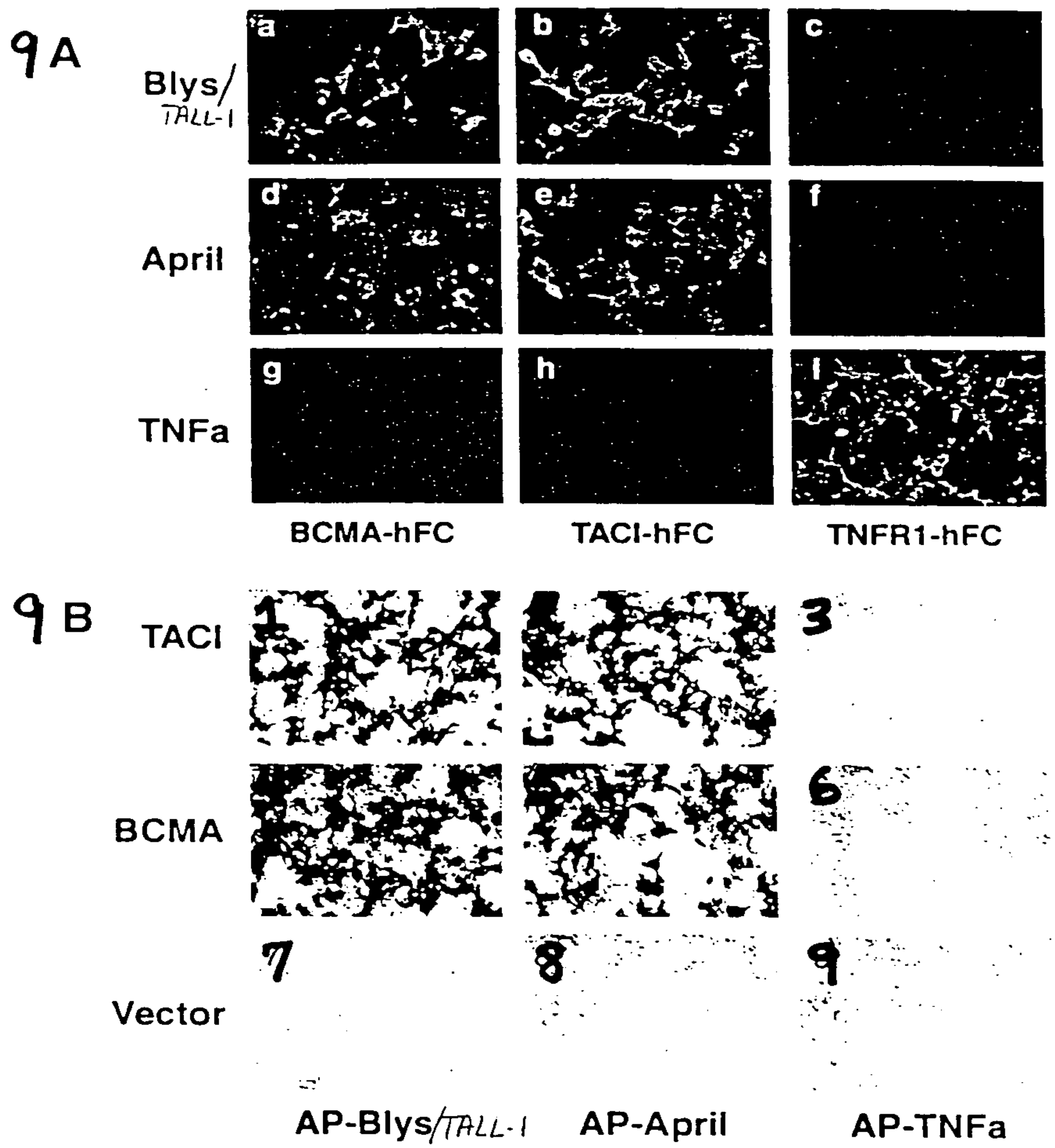

9A
Blys/ TALL-1
April
TNFa
a
b
c
d
e
f
g
h
i
BCMA-hFC
TACI-hFC
TNFR1-hFC
9B
TACI
BCMA
Vector
1
3
6
7
8
9
AP-Blys/TALL-1
AP-April
AP-TNFa

Fig. 9

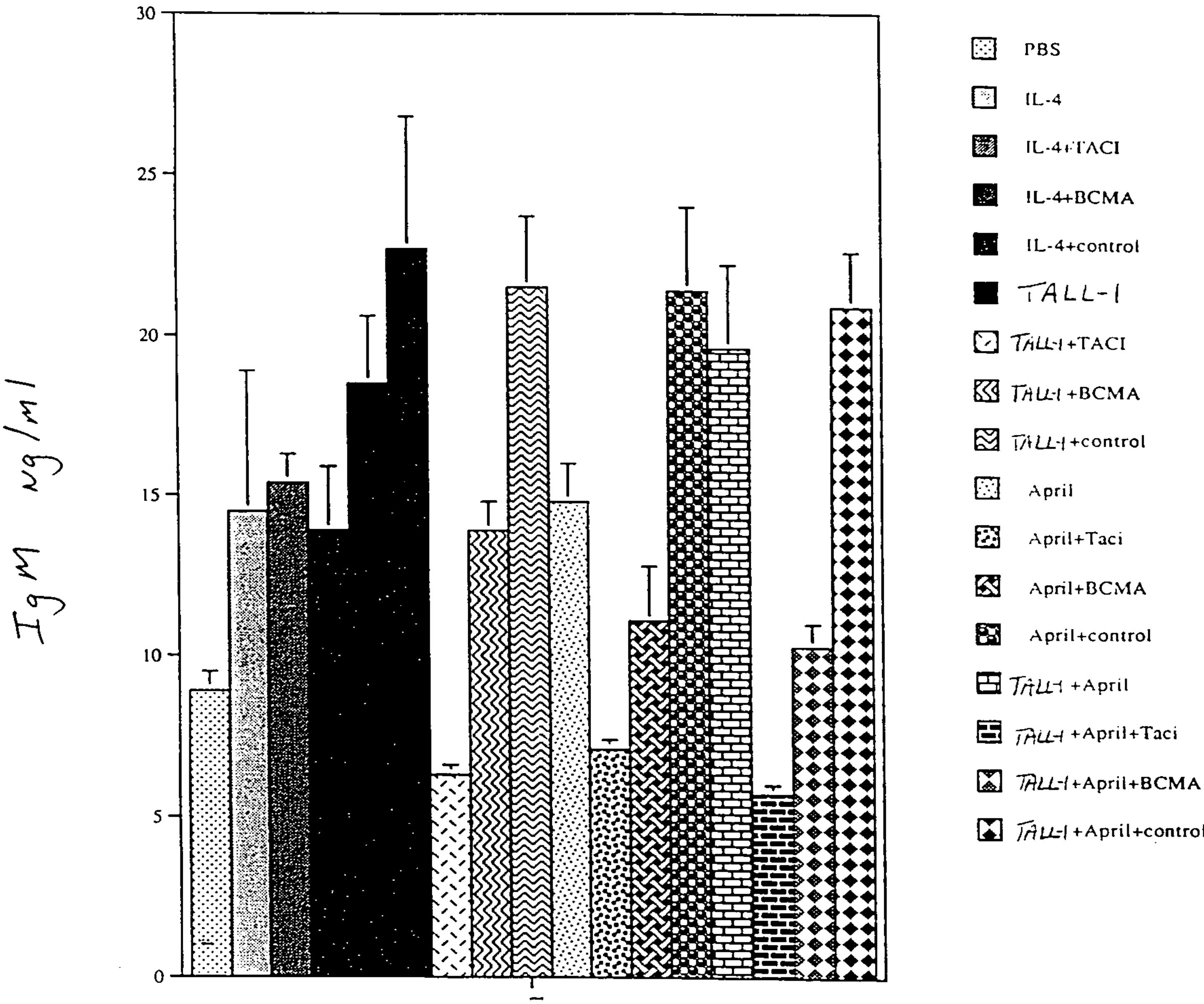

IgM ng/ml
30
25
20
15
10
5
0
PBS
IL-4
IL-4+TACI
IL-4+BCMA
IL-4+control
TALL-1
TALL-1+TACI
TALL-1+BCMA
TALL-1+control
April
April+Taci
April+BCMA
April+control
TALL-1 +April
TALL-1 +April+Taci
TALL-1+April+BCMA
TALL-1+April+control

Fig. 10

11A

11B

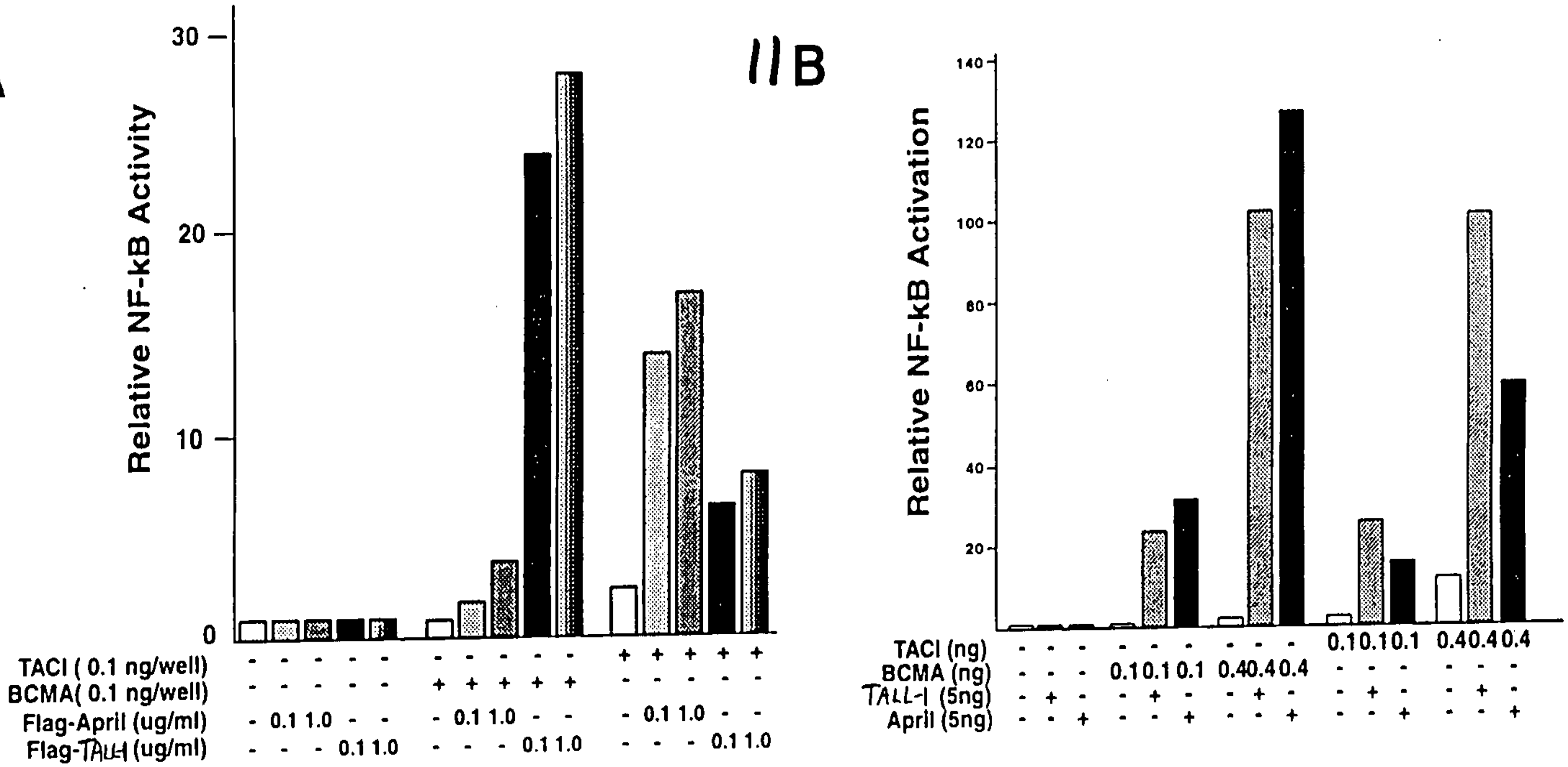
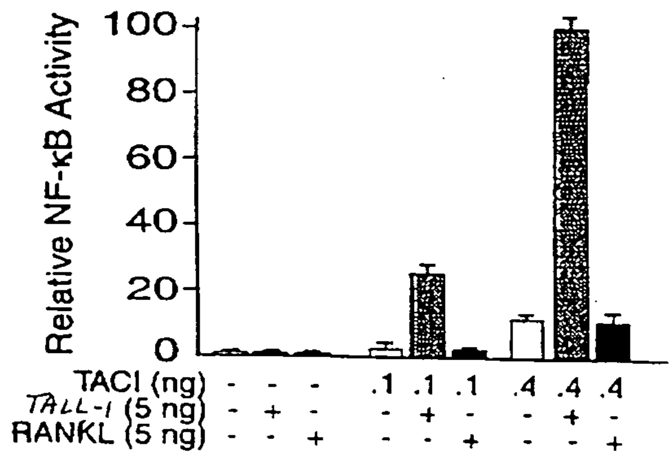


Fig 11

Fig. 11C



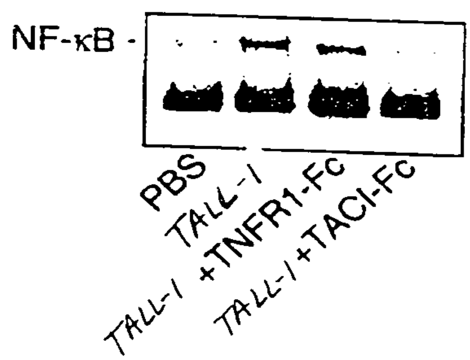


Fig. 11D

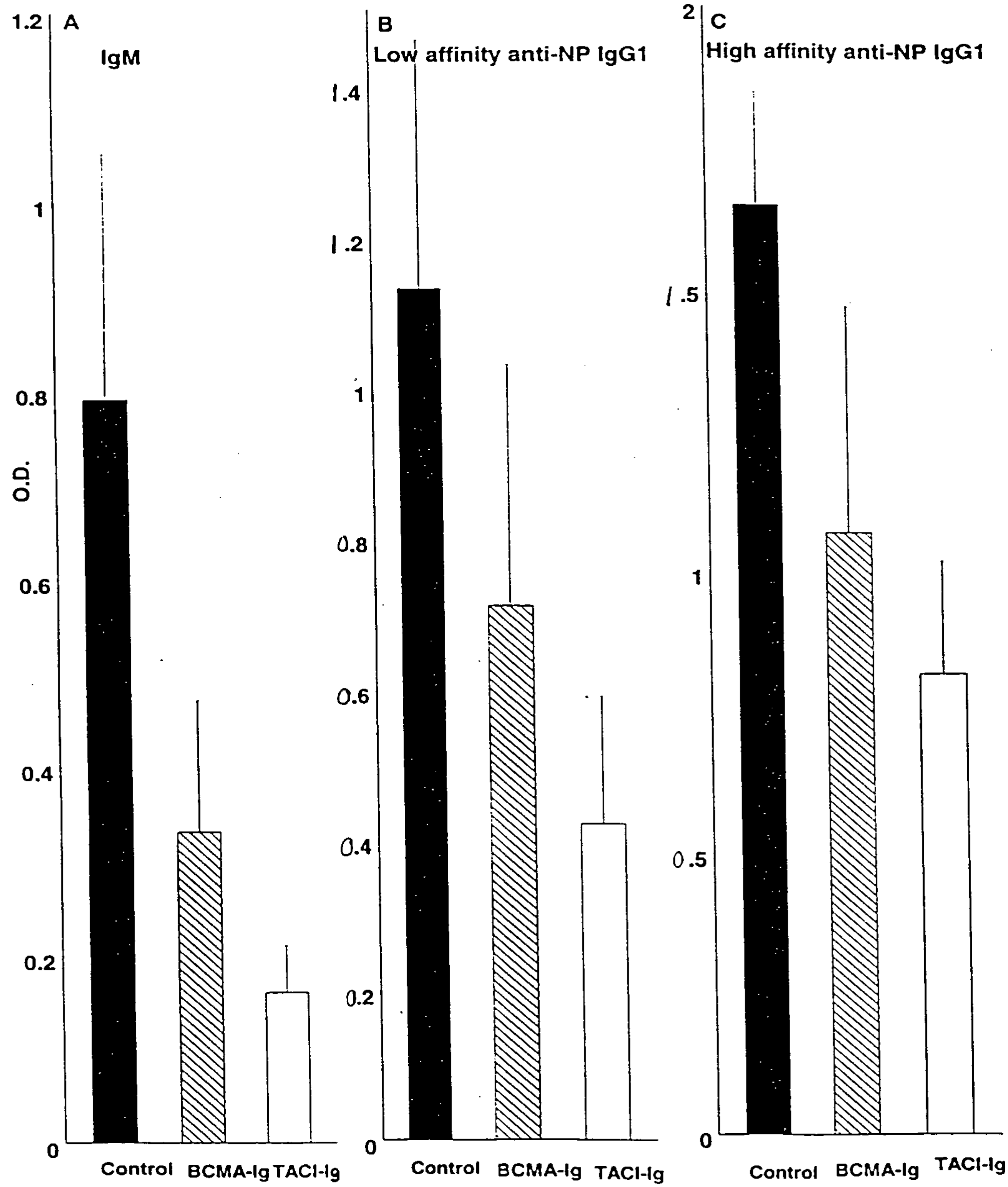

A
IgM
O.D.
1.2
1
0.8
0.6
0.4
0.2
0
Control
BCMA-Ig
TACI-Ig
B
Low affinity anti-NP IgG1
1.4
1.2
1
0.8
0.6
0.4
0.2
0
Control
BCMA-Ig
TACI-Ig
C
High affinity anti-NP IgG1
2
1.5
1
0.5
0
Control
BCMA-Ig
TACI-Ig

Fig. 12

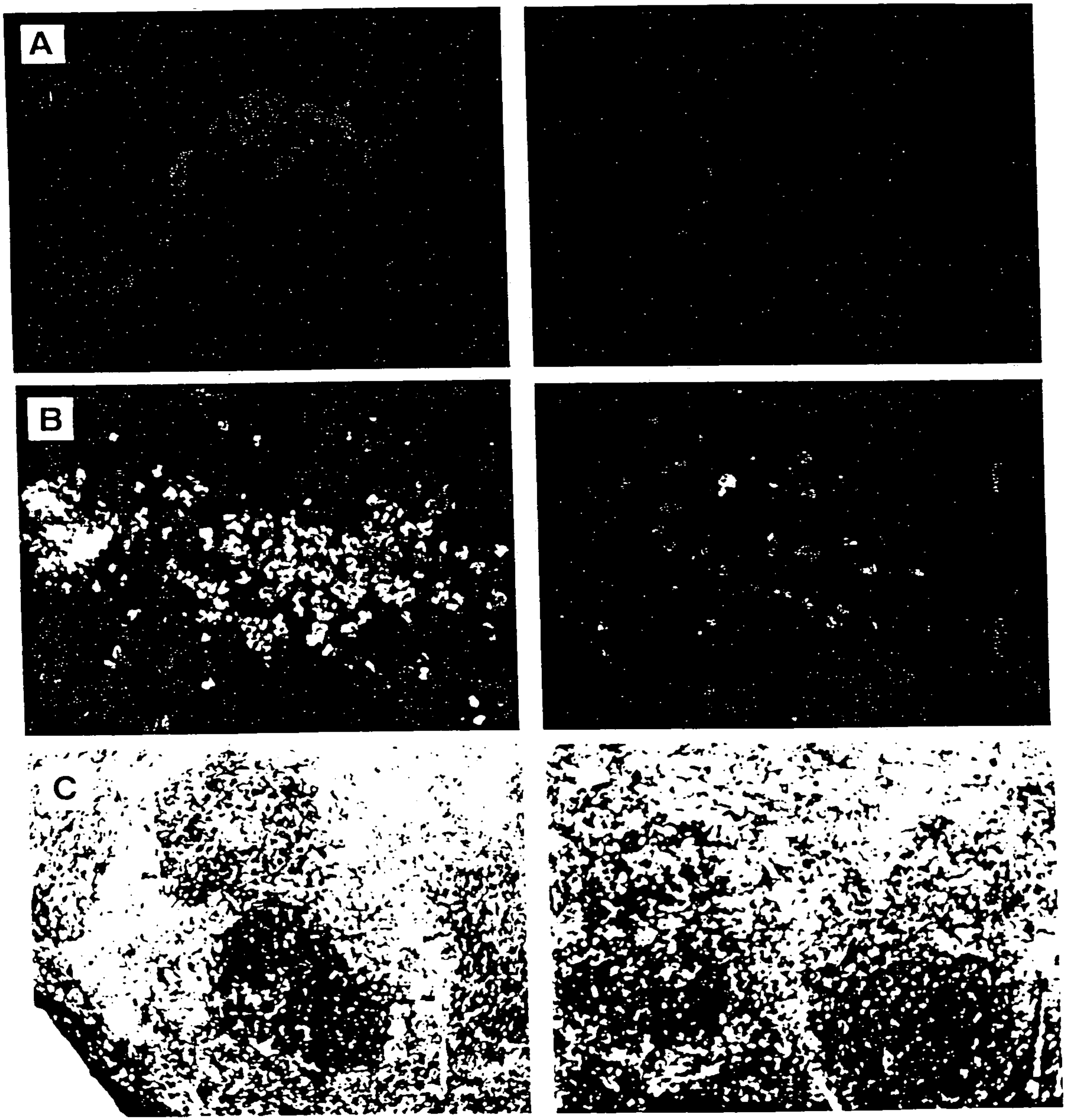


Fig. 13-1

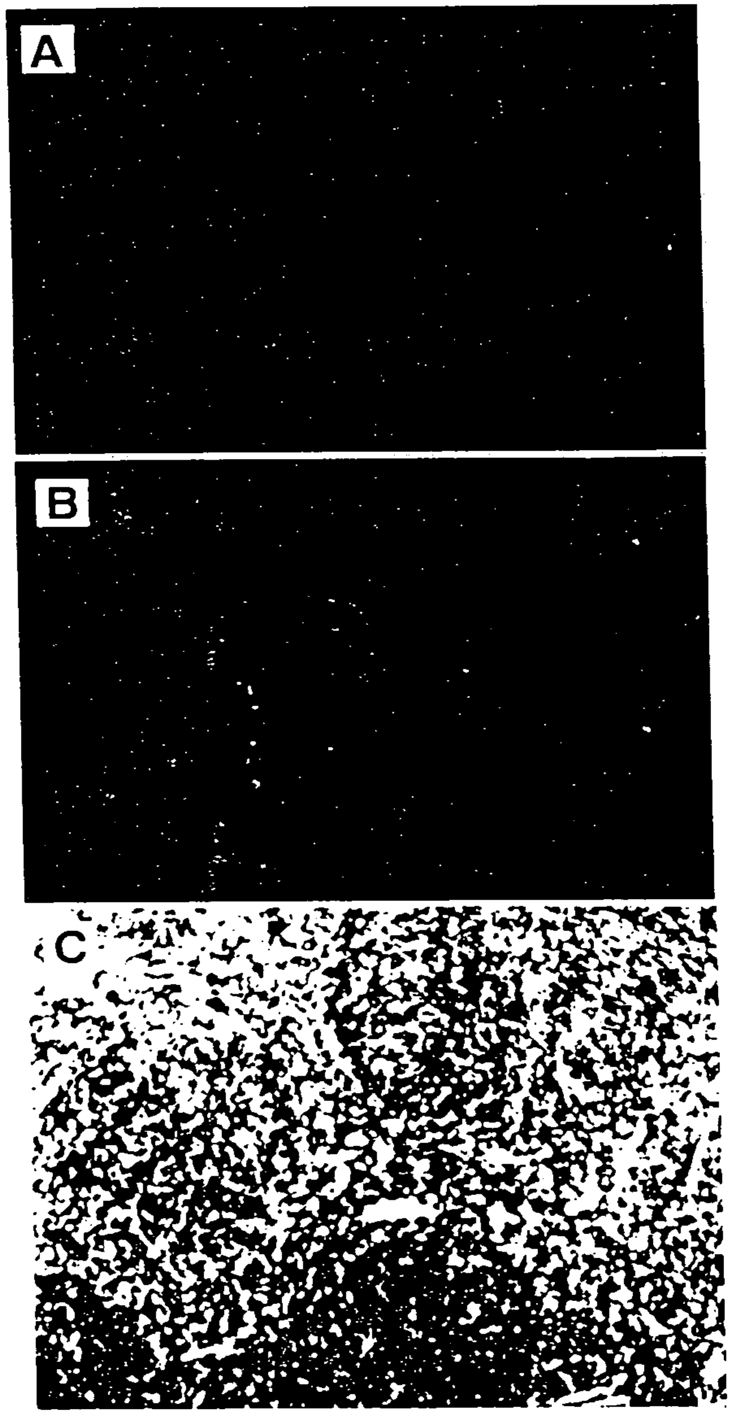


Fig. 13-2

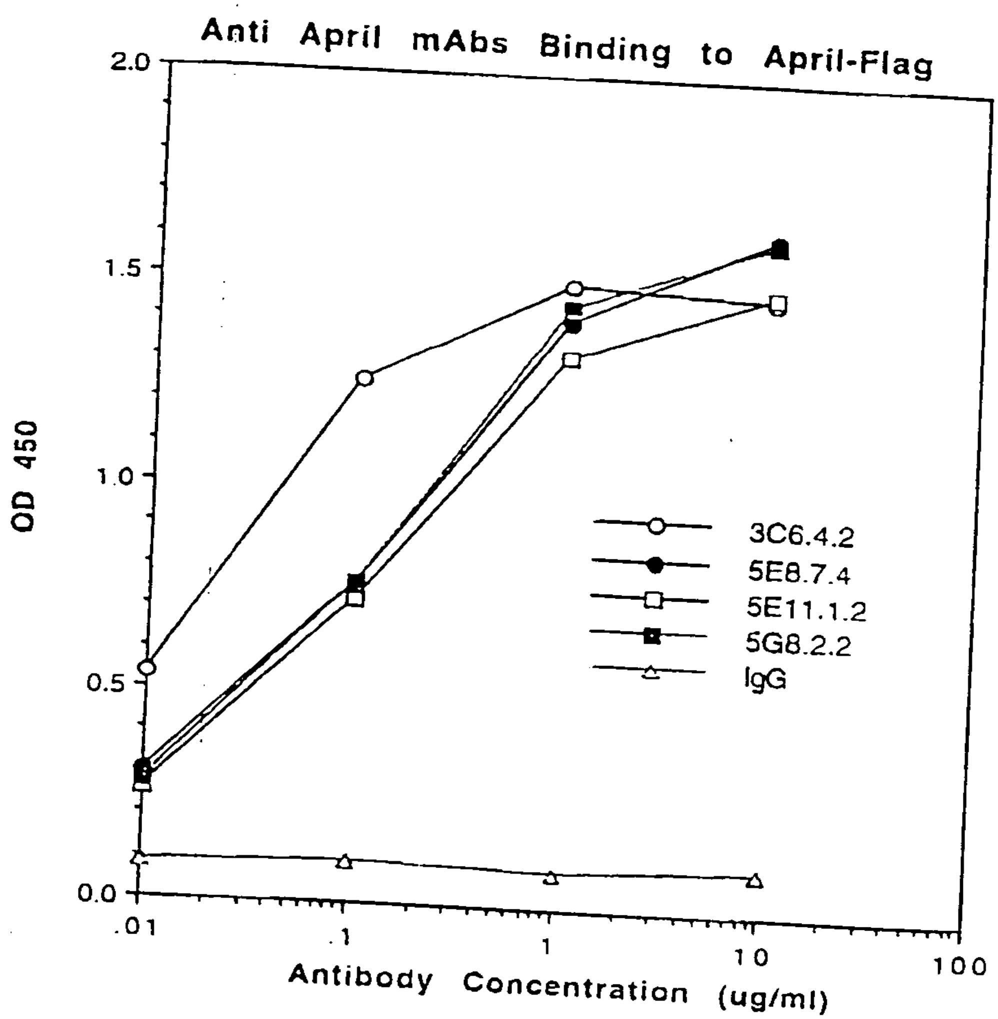

Anti April mAbs Binding to April-Flag
2.0
1.5
1.0
0.5
0.0
OD 450
3C6.4.2
5E8.7.4
5E11.1.2
5G8.2.2
IgG
.01
.1
1
10
100
Antibody Concentration (ug/ml)

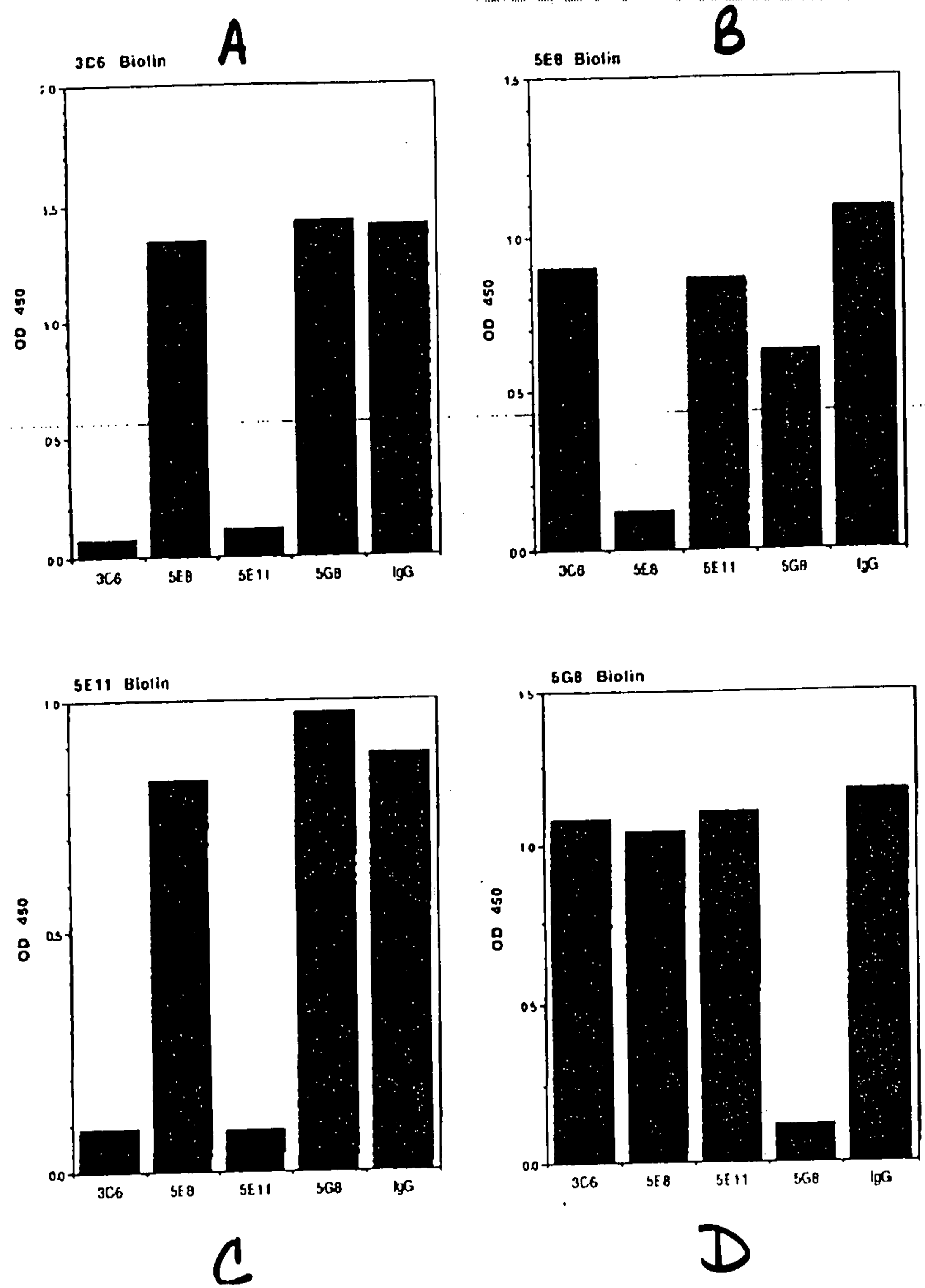
Fig. 14A

Summary of antiApril mABs

mAb	Isotype	Epitope	Binding (ELISA)		Block April bindiong to	
			April	TALL	BCMA	TACI
3C6.4.2	IgG2a	C	++	-	+++	+
5E8.7.4	IgG2a	A	++	-	-	-
5E11.1.2	IgG1	C?	++	-	+	+
5G8.2.2	IgG2a	B	++	-	-	-

MAb 5E11.1.2 may bind to the similar epitope.

Fig. 14B



A
3C6 Biotin
OD 450
0.0
0.5
1.0
1.5
2.0
3C6
5E8
5E11
5G8
IgG
B
5E8 Biotin
OD 450
0.0
0.5
1.0
1.5
3C6
5E8
5E11
5G8
IgG
C
5E11 Biotin
OD 450
0.0
0.5
1.0
3C6
5E8
5E11
5G8
IgG
D
5G8 Biotin
OD 450
0.0
0.5
1.0
1.5
3C6
5E8
5E11
5G8
IgG

Fig. 15

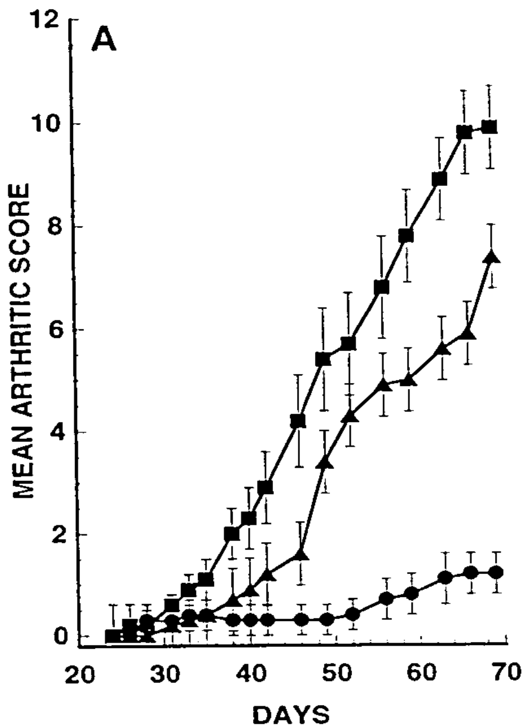


Fig. 16A

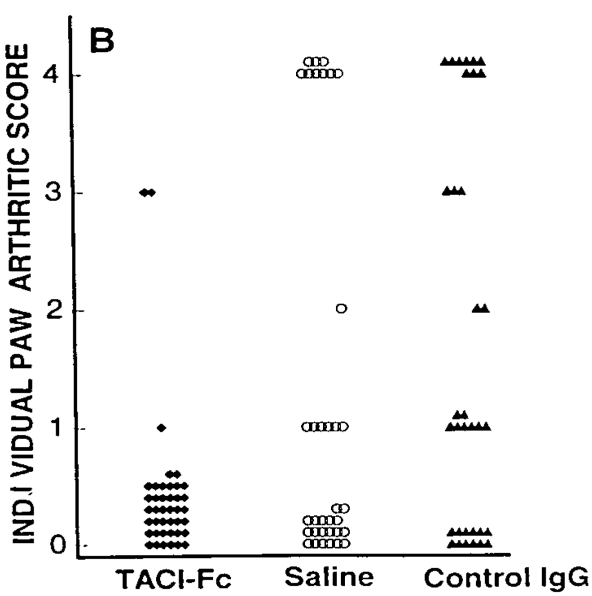


Fig. 16B

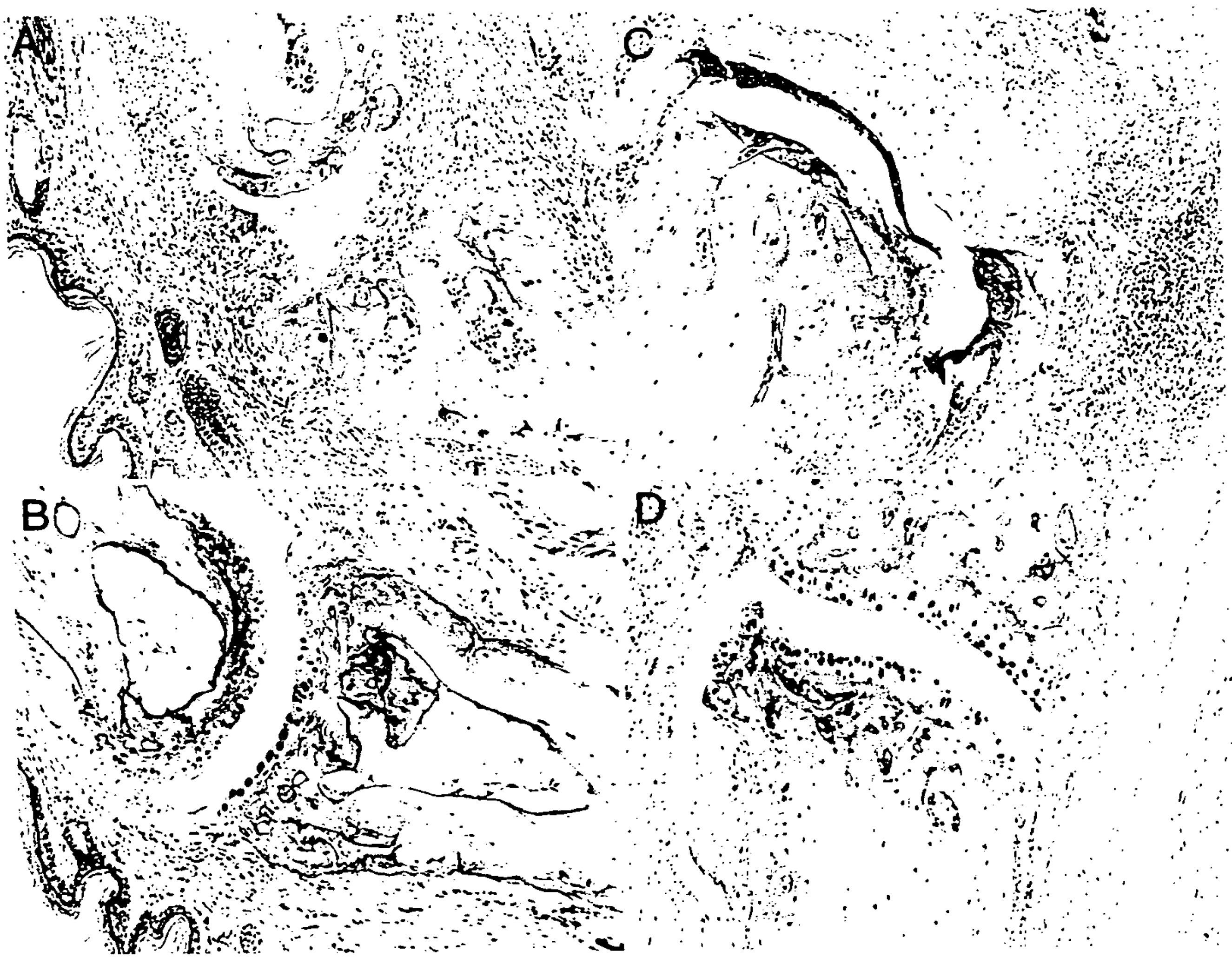


Fig. 17A-D

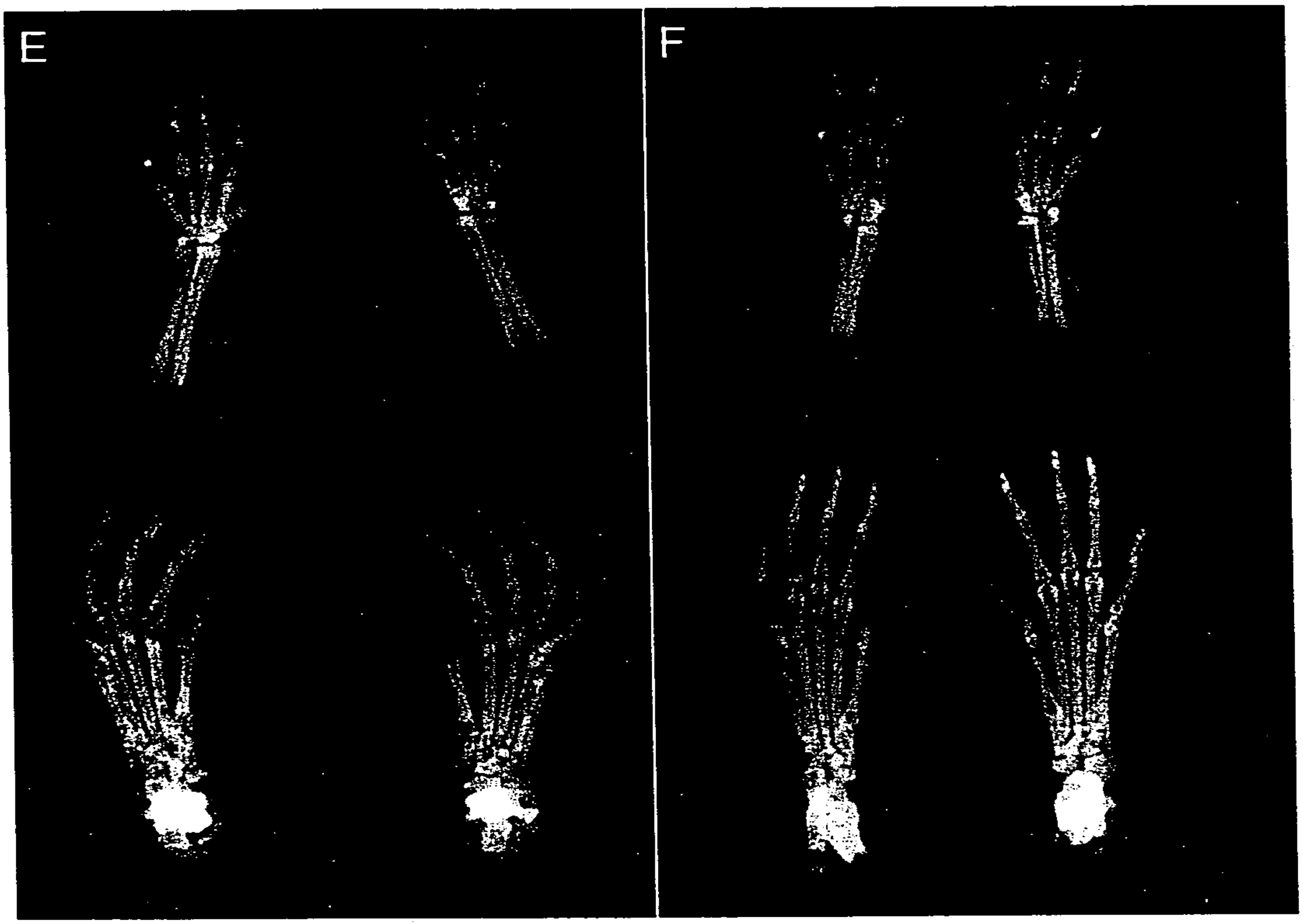


Fig. 17E-F

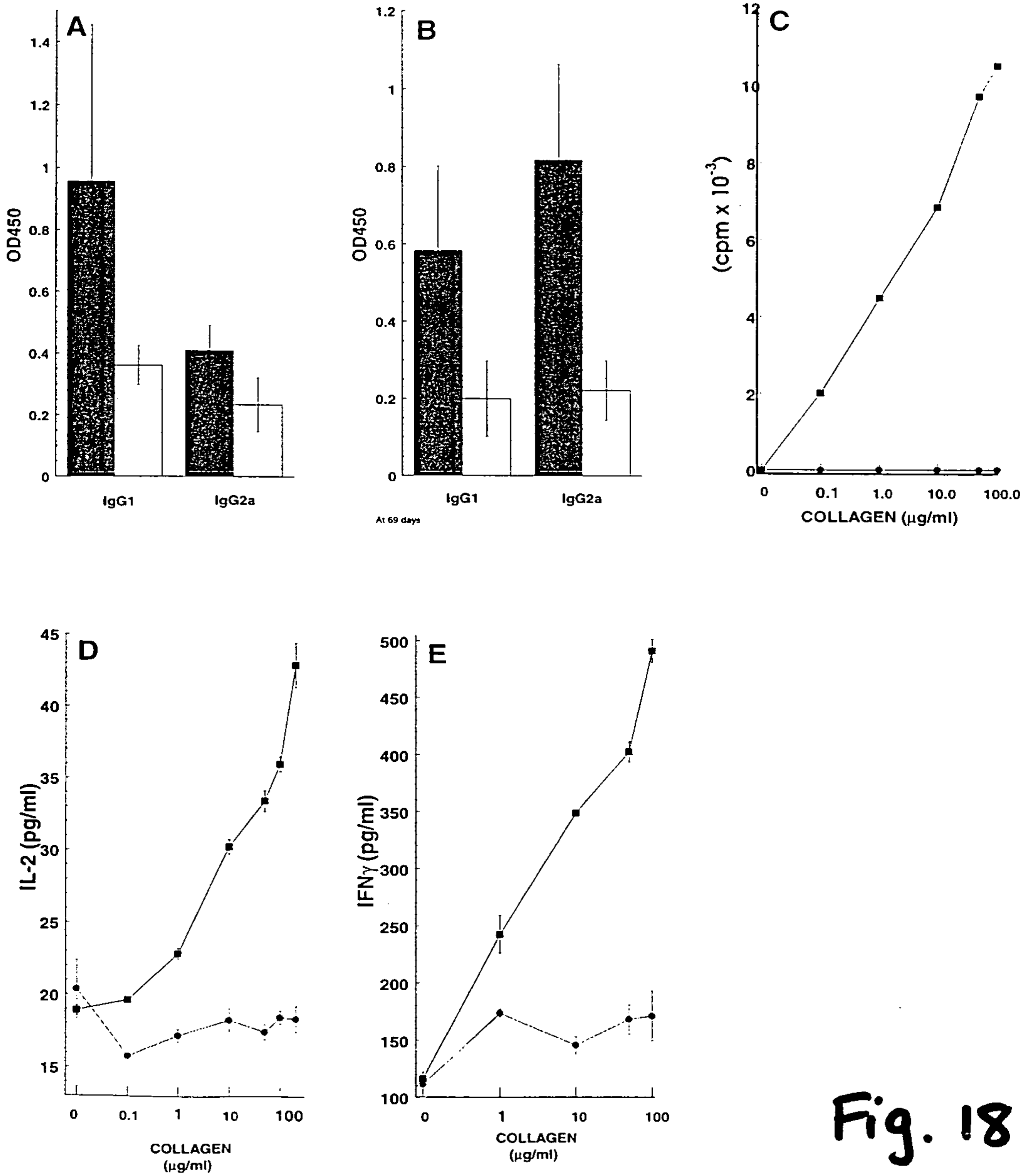

A
OD450
1.4
1.2
1
0.8
0.6
0.4
0.2
0
IgG1
IgG2a
B
OD450
1.2
1
0.8
0.6
0.4
0.2
0
IgG1
IgG2a
At 69 days
C
(cpm x 10^{-3})
12
10
8
6
4
2
0
0
0.1
1.0
10.0
100.0
COLLAGEN (µg/ml)
D
IL-2 (pg/ml)
45
40
35
30
25
20
15
0
0.1
1
10
100
COLLAGEN
(µg/ml)
E
IFNγ (pg/ml)
500
450
400
350
300
250
200
150
100
0
1
10
100
COLLAGEN
(µg/ml)

Fig. 18

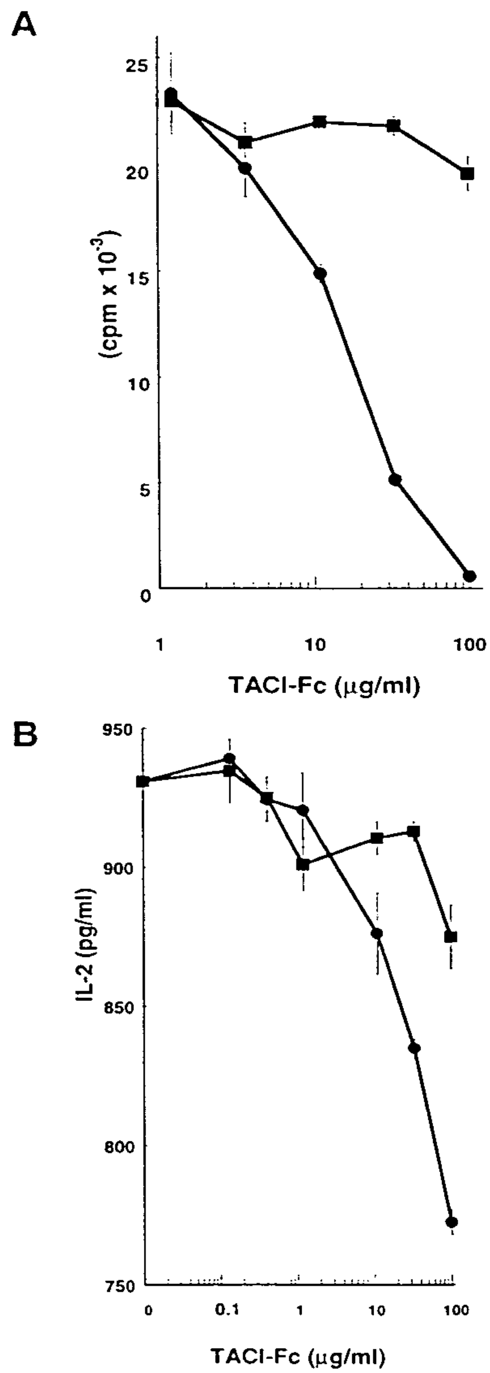

A
(cpm x 10^{-3})
25
20
15
10
5
0
1
10
100
TACI-Fc (μg/ml)
B
IL-2 (pg/ml)
950
900
850
800
750
0
0.1
1
10
100
TACI-Fc (μg/ml)

Fig. 19

TACI-Fc treatment of mice inhibits EAE in MBP-TCR transgenic mice

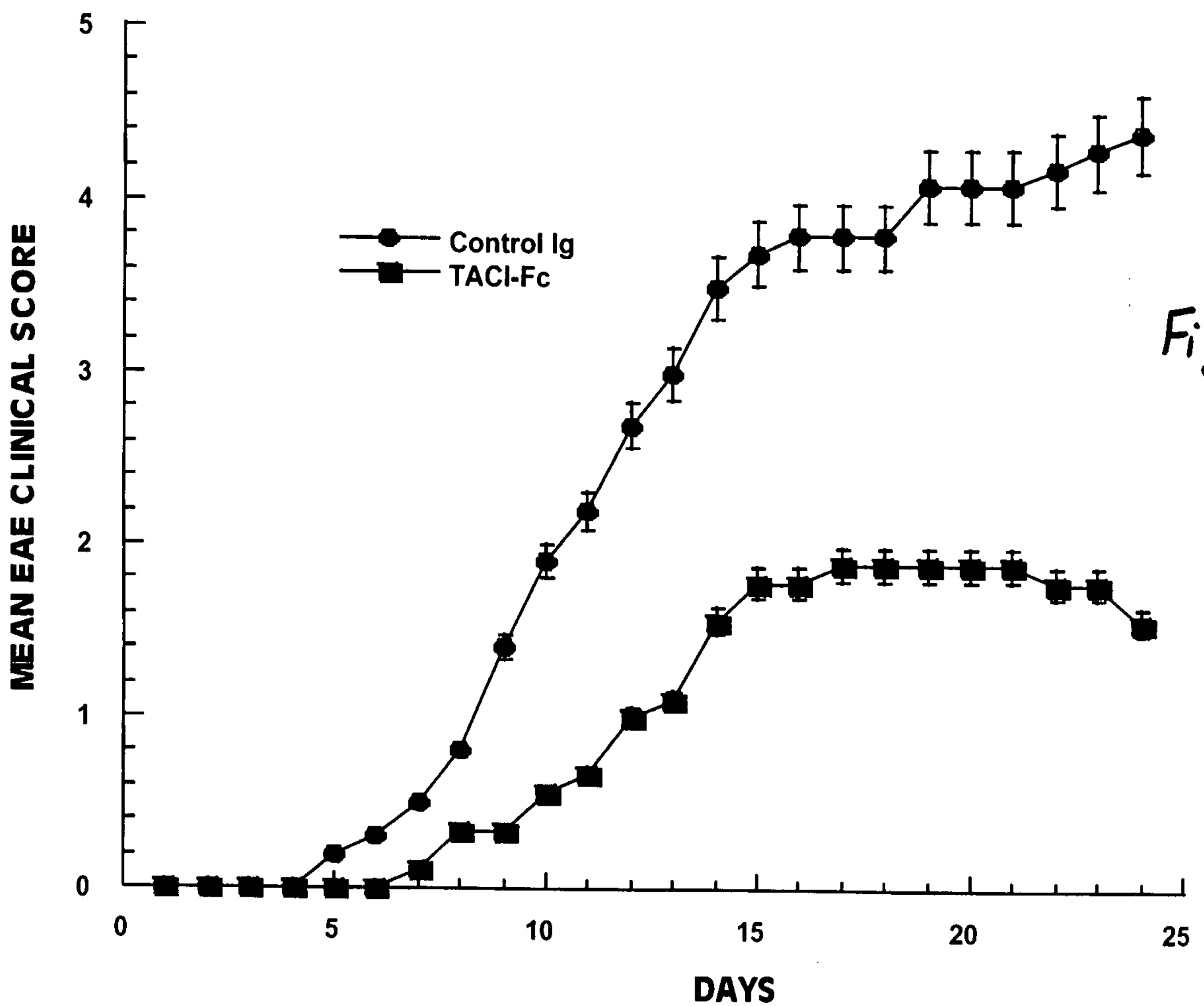


Fig. 20